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 NEWS 24   AUG 15  CAplus currency for Korean patents enhanced
 NEWS 25   AUG 25  CA/CAplus, CASREACT, and IFI and USPAT databases
                   enhanced for more flexible patent number searching
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=> s c myc
L1       43807 C MYC

=> s mRNA (3a) instabi?
L2         964 MRNA (3A) INSTABI?
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=> s l1 and l2
L3          29 L1 AND L2

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4           15 DUP REM L3 (14 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 15 ANSWERS - CONTINUE? Y/(N):y

L4   ANSWER 1 OF 15  CAPLUS  COPYRIGHT 2008 ACS on STN
AN   2004:999715  CAPLUS
DN   141:406751
TI   Assay and expression systems comprising reporter gene and
instability
     sequence DNA for identifying compounds which affect stability of
mRNA
IN   Kastelic, Tania; Cheneval, Dominique
PA   Novation Pharmaceuticals Inc., Can.
SO   U.S. Pat. Appl. Publ., 49 pp., Cont.-in-part of U.S. Ser. No.
869,159.
     CODEN: USXXCO
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.          KIND   DATE        APPLICATION NO.
DATE
     --------------      ----   --------    --------------------
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PI   US 20040231007       A1    20041118    US 2004-814634
20040401
     WO 2000039314        A1    20000706    WO 1999-CA1235
19991223
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN,
CR, CU,
             CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
ID, IL,
             IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
LV, MA,
             MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,
SG, SI,
             SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA,
ZW
         RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE,
             DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF,
BJ, CF,
             CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     AU 2005229165        A1    20051013    AU 2005-229165
20050401
     CA 2603585           A1    20051013    CA 2005-2603585
20050401
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WO 2005095615 A1 20051013 WO 2005-CA491
20050401
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ,
CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR,
KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NA, NI,
NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK,
SL, SM,
SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU,
ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM,
ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ,
DE, DK,
EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL,
PL, PT,
RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, ML,
MR, NE, SN, TD, TG
EP 1774000 A1 20070418 EP 2005-730094
20050401
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR,
HU, IE,
IS, IT, LI, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR
JP 2007530058 T 20071101 JP 2007-505349
20050401
US 20070190532 A1 20070816 US 2007-594851
20070504
PRAI GB 1998-28709 A 19981224
WO 1999-CA1235 W 19991223
US 2001-869159 A2 20010815
US 2004-814634 A 20040401
WO 2005-CA491 W 20050401

AB The present invention relates to an assay for the identification of biol.
active compds., in particular to a reporter gene assay for the identification of compds., which have an effect on mRNA stability. More
particularly, the present invention relates to a reporter gene expression
system and cell lines comprising said expression system. The invention
further relates to compds. which destabilize mRNA. Radicicol and radicicol analog A showed a clear effect on mRNA stability. Human APP,
Bcl-2α, c-myc, TNFα, IL-1β, VEGF
instability sequence were constructed. Instability sequence DNA is from

The gene encoding a cytokine, a gene encoding a chemokine, a gene encoding a nuclear transcription factor, a gene encoding an oxygenase, a proto-oncogene, an immediate early gene, a cell cycle controlling gene, and a gene involved in apoptosis.

L4 ANSWER 2 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 1
AN 2004:95192 BIOSIS
DN PREV200400084197
TI Mammary tumor induction in transgenic mice expressing an RNA-binding protein.
AU Tessier, Charles R.; Doyle, Glenn A.; Clark, Brad A.; Pitot, Henry C.; Ross, Jeff [Reprint Author]
CS McArdle Laboratory for Cancer Research, University of Wisconsin-Madison, 1400 University Avenue, Madison, WI, 53706, USA ross@oncology.wisc.edu
SO Cancer Research, (January 1 2004) Vol. 64, No. 1, pp. 209-214. print. ISSN: 0008-5472 (ISSN print).
DT Article
LA English
ED Entered STN: 11 Feb 2004
Last Updated on STN: 11 Feb 2004
AB We have analyzed mammary tumors arising in transgenic mice expressing a novel, multifunctional RNA-binding protein. The protein, which we call the c-myc mRNA coding region instability determinant binding protein (CRD-BP), binds to c-myc, insulin-like growth factor II, and beta-actin mRNAs, and to H19 RNA. Depending on the RNA substrate, the CRD-BP affects RNA localization, translation, or stability. CRD-BP levels are high during fetal development but low or undetectable in normal adult tissues. The CRD-BP is linked to tumorigenesis, because its expression is reactivated in some adult human breast, colon, and lung tumors. These data suggest the CRD-BP is a proto-oncogene. To test this idea, the CRD-BP was expressed from the whey acidic protein (WAP) promoter in mammary epithelial cells of adult transgenic mice. The incidence of mammary tumors was 95% and 60% in two lines of WAP-CRD-BP mice with high

and low relative CRD-BP expression, respectively. Some of the tumors metastasized. Nontransgenic mice did not develop mammary tumors. H19 RNA and insulin-like growth factor II mRNA were up-regulated significantly in non-neoplastic WAP-CRD-BP mammary tissue. WAP-CRD-BP mice are a novel model for mammary neoplasia and might provide insights into human breast cancer biology.

L4 ANSWER 3 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 2
AN 2003:399109 BIOSIS
DN PREV200300399109
TI CRD-BP: A c-myc mRNA stabilizing protein with an oncofetal pattern of expression.
AU Ioannidis, P. [Reprint Author]; Mahaira, L.; Papadopoulou, A.; Teixeira, M. R.; Heim, S.; Andersen, J. A.; Evangelou, E.; Dafni, U.; Pandis, N.; Trangas, T.
CS Immunology Center, St Savvas Hospital, 171 Alexandras Ave, Athens, 11522, Greece
pioannidis@ath.forthnet.gr
SO Anticancer Research, (May-June 2003) Vol. 23, No. 3A, pp. 2179-2184.
print.
CODEN: ANTRD4. ISSN: 0250-7005.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 27 Aug 2003
Last Updated on STN: 27 Aug 2003
AB The Coding Region Determinant-Binding Protein (CRD-BP) is an RRM and KH-domain-containing protein that recognizes specifically at least three RNAs. It binds to one of the two c-myc mRNA instability elements, to the 5'Un Translated Region (UTR) of the leader 3 IGF-II mRNA and to the oncofetal H19 RNA. CRD-BP has been assigned a role in stabilizing c-myc mRNA by preventing its endonucleolytic cleavage and in repressing the translation of the leader 3 IGF-II mRNA, the major embryonic species of this message.
CRD-BP is normally expressed only in fetal tissues. However, its expression is detected in primary tumors and transformed cell lines of

different origins. The vast majority of colon (80%) and breast (60%)
tumors and sarcomas (73%) express CRD-BP whereas in other tumor types, for
example prostate carcinomas, its expression is rare. CRD-BP expression
has also been detected in benign tumors such as breast fibroadenomas,
meningiomas and other benign mesenchymal tumors, implying a role for this
gene in abnormal cell proliferation. In breast carcinomas, CRD-BP
expression and or gene copy number gains in the region encompassing the
c-myc locus were detected in approximately 75% of
tumors, implying that the deregulated expression of c-
myc may be more widespread than previously believed. Infiltrated
lymph nodes, corresponding to CRD-BP- positive primary tumors, were also
found positive indicating that monitoring for CRD-BP could prove useful
for the detection and monitoring of disseminated disease.

L4 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:430571 CAPLUS
DN 137:151401
TI Regulation of c-myc mRNA decay by translational
pausing in a coding region instability determinant
AU Lemm, Ira; Ross, Jeff
CS McArdle Laboratory for Cancer Research, University of Wisconsin-Madison,
Madison, WI, 53706, USA
SO Molecular and Cellular Biology (2002), 22(12), 3959-3969
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB A 249-nucleotide coding region instability determinant (CRD) destabilizes
c-myc mRNA. Previous expts. identified a CRD-binding
protein (CRD-BP) that appears to protect the CRD from endonuclease
cleavage. However, it was unclear why a CRD-BP is required to protect a
well-translated mRNA whose coding region is covered with ribosomes. We
hypothesized that translational pausing in the CRD generates a
ribosome-deficient region downstream of the pause site, and this region is
exposed to endonuclease attack unless it is shielded by the CRD-BP.
Transfection and cell-free translation expts. reported here support this

hypothesis. Ribosome pausing occurs within the c-myc CRD in tRNA-depleted reticulocyte translation reactions. The pause sites map to a rare arginine (CGA) codon and to an adjacent threonine (ACA) codon. Changing these codons to more common codons increases translational efficiency in vitro and increases mRNA abundance in transfected cells. These data suggest that c-myc mRNA is rapidly degraded unless it is (i) translated without pausing or (ii) protected by the CRD-BP when pausing occurs. Addnl. mapping expts. suggest that the CRD is bipartite, with several upstream translation pause sites and a downstream endonuclease cleavage site.
RE.CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AN 2002:308512 BIOSIS
DN PREV200200308512
TI Correlation between intrinsic mRNA stability and the affinity of AUF1 (hnRNP D) and HuR for A+U-rich mRNAs.
AU Blaxall, Burns C.; Pende, Aldo; Wu, Steven C.; Port, J. David [Reprint author]
CS Division of Cardiology, University of Colorado HSC, 4200 East Ninth Avenue, B139, Denver, CO, 80262, USA
david.port@uchsc.edu
SO Molecular and Cellular Biochemistry, (March, 2002) Vol. 232, No. 1-2, pp. 1-11. print.
CODEN: MCBIB8. ISSN: 0300-8177.
DT Article
LA English
ED Entered STN: 22 May 2002
Last Updated on STN: 22 May 2002
AB Presence of A+U-rich elements (AREs) within 3'-untranslated regions (3'UTRs) of numerous mRNAs has been associated with rapid mRNA turnover; however, the interaction of specific factors with AREs is also associated with mRNA stabilization. Recently, two ARE binding proteins with putative mRNA destabilizing (AUF1) and stabilizing (HuR) properties have been described. However, no direct comparison of AUF1 and HuR binding properties has been made. Therefore, we examined the relative affinities

of p37AUF1 and HuR for a diverse set of ARE-containing mRNAs encoding beta-adrenergic receptors, a proto-oncogene, and a cytokine. We find that high-affinity AUF1 binding appears to require elements beyond primary nucleotide sequence. In contrast, binding of HuR appears considerably less constrained. As a functional correlate, we determined the ability of these specific mRNA sequences to affect the stability of chimeric beta-globin mRNA constructs. Although the relative affinity of AUF1 and HuR are generally predictive of mRNA stability, we find that certain mRNA sequences do not conform to these generalizations.

L4 ANSWER 6 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 3
AN 2001:313891 BIOSIS
DN PREV200100313891
TI mRNA localization by a 145-nucleotide region of the c-fos 3'-untranslated region: Links to translation but not stability.
AU Dalgleish, Gillian; Veyrune, Jean-Luc; Blanchard, Jean-Marie; Hesketh, John [Reprint author]
CS Rowett Research Institute, Bucksburn, Aberdeen, AB21 9SB, UK
j.e.hesketh@ncl.ac.uk
SO Journal of Biological Chemistry, (April 27, 2001) Vol. 276, No. 17, pp. 13593-13599. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 4 Jul 2001
Last Updated on STN: 19 Feb 2002
AB The presence of a localization signal in the 3'-untranslated region of c-fos mRNA was investigated by in situ hybridization and cell fractionation techniques. Cells were transfected with chimeric gene constructs in which the beta-globin coding region was used as a reporter and linked to either its own 3'-untranslated region, the c-fos 3'-untranslated region, or the c-fos 3'-untranslated region containing different deletions. Replacement of the endogenous beta-globin 3'-untranslated region by that from c-fos caused a redistribution of the transcripts so that they were recovered in cytoskeletal-bound polysomes

and seen localized in the perinuclear cytoplasm. Deletion of the AU-rich instability region did not affect transcript localization, but removal of a distinct 145-nucleotide region of the 3'-untranslated region abolished it. The prevention of transcript translation by desferrioxamine led to a marked loss of transcript localization, independent of mRNA instability. The data show that the 3'-untranslated region of c-fos mRNA, as c-myc, contains a localization signal, which targets the mRNA to the perinuclear cytoskeleton. We propose that this is important to ensure efficient nuclear import of these key regulatory proteins. mRNA localization by the fos 3'-untranslated region is independent of mRNA instability, and the two are determined by different regulatory elements.

L4 ANSWER 7 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 4
AN 1997:226015 BIOSIS
DN PREV199799517731
TI Identification of two proteins that bind to a pyrimidine-rich sequence in the 3'-untranslated region of GAP-43 mRNA.
AU Irwin, Nina [Reprint author]; Baekelandt, Veerle; Goritchenko, Luda; Benowitz, Larry I.
CS Lab. Neurosci. Res. Neurosurg., Children's Hosp., En 308, 300 Longwood Ave., Boston, MA 02115, USA
SO Nucleic Acids Research, (1997) Vol. 25, No. 6, pp. 1281-1288. CODEN: NARHAD. ISSN: 0305-1048.
DT Article
LA English
ED Entered STN: 22 May 1997
Last Updated on STN: 22 May 1997
AB GAP-43 is a membrane phosphoprotein that is important for the development and plasticity of neural connections. In undifferentiated PC12 pheochromocytoma cells, GAP-43 mRNA degrades rapidly (t-1/2, = 5 h), but becomes stable when cells are treated with nerve growth factor. To identify trans-acting factors that may influence mRNA stability, we combined column chromatography and gel mobility shift assays to isolate GAP-43 mRNA binding proteins from neonatal bovine brain tissue. This

resulted in the isolation of two proteins that bind specifically and competitively to a pyrimidine-rich sequence in the 3'-untranslated region of GAP-43 mRNA. Partial amino acid sequencing revealed that one of the RNA binding proteins coincides with FBP (far upstream element binding protein), previously characterized as a protein that resembles hnRNP K and which binds to a single-stranded, pyrimidine-rich DNA sequence upstream of the c-myc gene to activate its expression. The other binding protein shares sequence homology with PTB, a polypyrimidine tract binding protein implicated in RNA splicing and regulation of translation initiation. The two proteins bind to a 26 nt pyrimidine-rich sequence lying 300 nt downstream of the end of the coding region, in an area shown by others to confer instability on a reporter mRNA in transient transfection assays. We therefore propose that FBP and the PTB-like protein may compete for binding at the same site to influence the stability of GAP-43 mRNA.

L4 ANSWER 8 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
DUPLICATE 5
AN 1996:364403 BIOSIS
DN PREV199699086759
TI Identification of sequences in c-myc mRNA that regulate its steady-state levels.
AU Yeilding, Newman M.; Rehman, Muhammad T.; Lee, William M. F. [Reprint author]
CS 663 CRB, 415 Curie Blvd., Univ. Pennsylvania, Philadelphia, PA 19104, USA
SO Molecular and Cellular Biology, (1996) Vol. 16, No. 7, pp. 3511-3522.
CODEN: MCEBD4. ISSN: 0270-7306.
DT Article
LA English
ED Entered STN: 14 Aug 1996
Last Updated on STN: 14 Aug 1996
AB The level of cellular myc proto-oncogene expression is rapidly regulated in response to environmental signals and influences cell proliferation and differentiation. Regulation is dependent on the fast turnover of

c-myc mRNA, which enables cells to rapidly alter c-myc mRNA levels. Efforts to identify elements in myc mRNA responsible for its instability have used a variety of approaches, all of which require manipulations that perturb normal cell metabolism. These various approaches have implicated different regions of the mRNA and have led to a lack of consensus over which regions actually dictate rapid turnover and low steady-state levels of c-myc mRNA. To identify these regions by an approach that does not perturb cell metabolism acutely and that directly assesses the effect of a c-myc mRNA region on the steady-state levels of c-myc mRNA, we developed an assay using reverse transcription and PCR to compare the steady-state levels of human myc mRNAs transcribed from two similarly constructed myc genes transiently cotransfected into proliferating C2C12 myoblasts. Deletion mutations were introduced into myc genes, and the levels of their mRNAs were compared with that of a near-normal, reference myc mRNA. Deletion of most of the myc 3' untranslated region (UTR) raised myc mRNA levels, while deletion of sequences in the myc 5' UTR (most of exon 1), exon 2, or the protein-coding region of exon 3 did not, thus demonstrating that the 3' UTR is responsible for keeping myc mRNA levels low. Using a similar reverse transcription-PCR assay for comparing the steady-state levels of two beta-globin-myc fusion mRNAs, we showed that fusion of the myc 3' UTR lowers globin mRNA levels by destabilizing beta-globin mRNA. Surprisingly, fusion of the protein-coding region of myc exon 3 also lowered globin mRNA steady-state levels. Investigating the possibility that exon 3 coding sequences may play some other role in regulating c-myc mRNA turnover, we demonstrated that these sequences, but not myc 3' UTR sequences, are necessary for the normal posttranscriptional downregulation of c-myc mRNA during myoblast differentiation. We conclude that, while two elements within c-myc mRNA can act as instability determinants in a heterologous context, only the instability element in the 3' UTR regulates its steady-state levels in

proliferating C2C12 cells.

L4 ANSWER 9 OF 15 EMBASE COPYRIGHT (c) 2008 Elsevier B.V. All rights reserved on STN
AN 1995141433 EMBASE
TI Expression of the blood-clotting factor-VIII cDNA is repressed by a tránscriptional silencer located in its coding region.
AU Hoeben, Rob C., Dr. (correspondence)
CS Lab. of Molecular Carcinogenesis, Department of Medical Biochemistry, Sylvius Laboratory, Wassenaarseweg 72, 2333 AL Leiden, Netherlands.
AU Fallaux, Frits J.; Cramer, Steve J.; Van Den Wollenberg, Diana J.M.; Van Ormondt, Hans; Briet, Ernest; Van Der Eb, Alex J.
SO Blood, (1 May 1995) Vol. 85, No. 9, pp. 2447-2454.
Refs: 39
ISSN: 0006-4971 CODEN: BLOOAW
CY United States
DT Journal; Article
FS 022 Human Genetics
025 Hematology
005 General Pathology and Pathological Anatomy
LA English
SL English
ED Entered STN: 31 May 1995
Last Updated on STN: 31 May 1995
AB Hemophilia A is caused by a deficiency of factor-VIII procoagulant (fVIII) activity. The current treatment by frequent infusions of plasma-derived fVIII concentrates is very effective but has the risk of transmittance of blood- borne viruses (human immunodeficiency virus [H/V], hepatitis viruses). Use of recombinant DNA-derived fVIII as well as gene therapy could make hemophilia treatment independent of blood-derived products. So far, the problematic production of the fVIII protein and the low titers of the fVIII retrovirus stocks have prevented preclinical trials of gene therapy for hemophilia A in large-animal models. We have initiated a study of the mechanisms that oppose efficient fVIII synthesis. We have established that fVIII cDNA contains sequences that dominantly inhibit its own expression from retroviral as well as from plasmid vectors. The

inhibition is not caused by instability of the fVIII mRNA (t(1/2), ±6 hours) but rather to repression at the level of transcription. A 305-bp fragment is identified that is involved in but not sufficient for repression. This fragment does not overlap the region recently identified by Lynch et al (Hum Gene Ther 4:259, 1993) as a dominant inhibitor of RNA accumulation. The repression is mediated by a cellular factor (or factors) and is independent of the orientation of the element in the transcription unit, giving the repressor element the hallmarks of a transcriptional silencer.

L4 ANSWER 10 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN DUPLICATE 6

AN 1993:209797 BIOSIS
DN PREV199395111022
TI 1,25-Dihydroxyvitamin D-3 destabilizes c-myc mRNA in HL-60 leukemic cells.
AU Mangasarian, Karen; Mellon, William S. [Reprint author]
CS University Wisconsin, School Pharmacy, 425 N. Charter St., Madison, WI 53706, USA
SO Biochimica et Biophysica Acta, (1993) Vol. 1172, No. 1-2, pp. 55-63.
CODEN: BBACAQ. ISSN: 0006-3002.
DT Article
LA English
ED Entered STN: 23 Apr 1993
Last Updated on STN: 23 Apr 1993
AB The differentiation process is accompanied by alterations in the expression of a variety of genes. Monocytic maturation of hematopoietic cells (HL-60) induced by 1,25-dihydroxyvitamin D-3 (1,25(OH)-2D-3), results in a decrease in steady state c-myc mRNA levels. To elucidate the mechanism by which 1,25(OH)-2D-3 regulates c-myc mRNA expression, transcriptional and post-transcriptional modes of regulation were investigated. No transcriptional regulation was identified, however, 1,25(OH)-2D-3 appeared to decrease steady state c-myc mRNA levels by increasing its turnover rate. Using actinomycin D to block transcription, the half-life of c-myc mRNA was shown to decrease from 20 min in the absence of 1,25(OH)-2D-3 to lt 5 min in the presence of

1,25(OH)-2D-3. Cycloheximide reversed the instability induced by 1,25(OH)-2D-3, prolonging the half-life of c-myc mRNA in both uninduced and 1,25(OH)-2D-3-induced HL60 cells to gt 60 min, indicating a translational requirement for the destabilization process. Additionally, the c-myc mRNA instability induced by 1,25(OH)-2D-3 in HL-60 appears to be a specific result of this agent, as indicated by the inability of other monocytic and granulocytic differentiation inducing agents to destabilize c-myc mRNA.

L4 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1992:230257 CAPLUS
DN 116:230257
OREF 116:38859a,38862a
TI What determines the instability of c-myc proto-oncogene mRNA?
AU Laird-Offringa, Ite A.
CS Dep. Microbiol. Mol. Genet., Harvard Med. Sch., Boston, MA, 02115, USA
SO BioEssays (1992), 14(2), 119-24
CODEN: BIOEEJ; ISSN: 0265-9247
DT Journal; General Review
LA English
AB A review with 38 refs. on the mechanism of degradation of c-myc mRNA, and its similarity with c-fos mRNA decay. The c-myc proto-oncogene is believed to be involved in the regulation of cell growth and differentiation. Deregulation of this gene, resulting in an inappropriate increase of gene product, can contribute to cancer formation. One of the ways in which the expression of the c-myc gene can be deregulated is by the stabilization of the labile c-myc mRNA. The rapid degradation of the c-myc transcripts appears to be mediated by at least 2 distinct regions in the mRNA. One lies in the 3' untranslated region, and presumably consists of (A+U)-rich sequences. The other lies in the C-terminal part of the coding region and colocalizes with sequences encoding protein-dimerization motifs. The exact mechanism by which the destabilizing elements function is not yet clear. Shortening of the poly(A) tail of the c-myc message appears to precede degradation of the transcript. When translation is blocked, this shortening is slowed down and the mRNA is stabilized. This suggests that deadenylation is required before degradation of the mRNA body can take place.

L4 ANSWER 12 OF 15 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on
STN DUPLICATE 7
AN 1991:340854 BIOSIS
DN PREV199192040229; BA92:40229
TI RAPID C-MYC MESSENGER RNA DEGRADATION DOES NOT REQUIRE A PLUS U-RICH SEQUENCES OR COMPLETE TRANSLATION OF THE MESSENGER RNA.
AU LAIRD-OFFRINGA I A [Reprint author]; ELFFERICH P; VAN DER EB A J
CS DEP MICROBIOL MOL GENET, HARVARD MED SCH, 200 LONGWOOD AVE, BOSTON, MASS
02115, USA
SO Nucleic Acids Research, (1991) Vol. 19, No. 9, pp. 2387-2394.
CODEN: NARHAD. ISSN: 0305-1048.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 31 Jul 1991
Last Updated on STN: 1 Aug 1991
AB The c-myc proto-oncogene encodes a highly unstable mRNA. Stabilized, turncated myc transcripts have been found in several human and murine tumors of hematopoietic origin. Recently, two tumors expressing 3' truncated c-myc mRNAs that were five times more stable than normal myc transcripts, were described. We have tried to determine the cause of the increased stability of the 3' truncated myc transcripts by studying the half-life of mutated c -myc mRNAs. The c-myc 3' untranslated region has been shown to contain sequences that confer mRNA instability. Possible candidates for such sequences are two (A + U)-rich regions in the 3' end of the c-myc RNA that resemble RNA destabilizing elements present in the c-fos and GMCSF mRNAs.
We show that deletions in the (A + U)-rich regions do not stabilize c-myc messengers, and that hybrid mRNAs containing SV40 sequences at their 3' ends and terminating at an SV40 polyadenylation signal decay as quickly as normal c-myc transcripts.
Our results indicate that neither the loss of (A + U)-rich sequences nor the mere addition of non-myc sequences to the 3' end of the mRNA lead to stabilization. We also show that rapid degradation of c-myc mRNA does not require complete translation of the coding sequences.

L4 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1991:56810 CAPLUS

DN 114:56810
OREF 114:9641a,9644a
TI Cis-acting determinants required for c-myc
mRNA instability and their mechanistic implications
AU Mango, Susan Elizabeth
CS Princeton Univ., Princeton, NJ, USA
SO (1990) 133 pp. Avail.: Univ. Microfilms Int., Order No.
DA9027580
From: Diss. Abstr. Int. B 1990, 51(5), 2209-10
DT Dissertation
LA English
AB Unavailable

L4 ANSWER 14 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1989:52215 CAPLUS
DN 110:52215
OREF 110:8517a,8520a
TI Activation of the transforming potential of the human fos
proto-oncogene
requires message stabilization and results in increased amounts
of
partially modified fos protein
AU Lee, William M. F.; Lin, Chin; Curran, Tom
CS Cancer Res. Inst., Univ. California, San Francisco, CA, 94143,
USA
SO Molecular and Cellular Biology (1988), 8(12), 5521-7
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The requirements for activation of the transformation potential
of the
human c-fos proto-oncogene were investigated. Recombinant
plasmids containing
the Moloney murine leukemia virus long terminal repeat directing
transcription of the c-fos coding region and either the
authentic c-fos 3'
untranslated region (UTR) or the 3' UTR from human c-myc
were inefficient at inducing transformation. In contrast, a
recombinant
that substituted most of the c-fos 3' UTR with the 3' portion of
the
simian virus 40 T-antigen gene transformed cells well. This
difference in
transformation efficiency appeared to be due to significantly
higher
levels of fos mRNA and protein expressed from the transforming
recombinant. This, in turn, was due to the much greater
stability of its
mRNA compared with those from the poorly transforming
recombinants containing
the c-fos or c-myc 3' UTR. Thus, the 3' UTR of the
human c-fos mRNA is responsible for its rapid degradation and
limits the

steady-state levels of transcript and protein. Cells transformed by the activated human c-fos plasmids contained increased amts. of partially modified c-fos protein (c-Fos). This form of c-fos turned over much more rapidly than the highly modified form of c-fos induced by serum stimulation.

L4 ANSWER 15 OF 15 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1985:22195 CAPLUS
DN 102:22195
OREF 102:3645a,3648a
TI Extreme instability of myc mRNA in normal and transformed human cells
AU Dani, C.; Blanchard, J. M.; Piechaczyk, M.; El Sabouty, S.; Marty, L.; Jeanteur, P.
CS Lab. Biol. Mol., Univ. Sci. Tech. Languedoc, Montpellier, 34060, Fr.
SO Proceedings of the National Academy of Sciences of the United States of America (1984), 81(22), 7046-50
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB To address the possibility that the expression of the myc gene might be regulated at a post-transcriptional level, the half-life of myc mRNA in various cells was investigated. The survey included normal human embryonic fibroblasts as well as transformed human cells of various origins: cervix carcinoma (HeLa), breast carcinoma (MCF7), Burkitt lymphoma (Daudi), and promyelocytic leukemia (HL60). All these cells revealed an extreme instability of myc mRNA (half-life, .apprx.10 min), suggesting that the control of myc mRNA degradation might be a general means (although not necessarily exclusive) of regulating both the level and the timing of myc gene expression. Inhibition of protein synthesis resulted in a dramatic stabilization of myc mRNA in HeLa, MCF7, and HL60 cells, suggesting that the controlling element might itself be, at least in these cells, a protein of rapid turnover. This finding opens the way to studying the mechanism of myc mRNA inactivation in these different cell types. However, protein

synthesis inhibition had no effect on myc mRNA
instability in other transformed (Daudi) cells lines as well as
normal embryonic human fibroblasts. These different types of behavior
suggest that the post-transcriptional control of myc gene expression might
involve multiple factors that would be differently affected in various
cell types.

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CA SUBSCRIBER PRICE	0.00	

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